

PA (INTE-) Integrated genetics.
PI Beck AK, Withey RM, Zaborecky JR, Massiello NC;

Best local Similarity 27.6%; Pred. No. 5.15e-02;
 Matches 27; Conservative 27; Mismatches 41; Indels 3; Gaps 3;

PT Recombinant human erythropoietin - produced by a transformed rodent
 PT capable of producing N-linked and O-linked glycosylated human
 PT erythropoietin.
 PS disclosure; p; English.
 CC EPO 104B was one of four positive clones isolated from a cDNA
 CC library prep. from mRNA extracted from a human fetus of about 20
 CC wk. gestation. The clone was identified using two probes, EPO11 and
 CC EPO2 based on the published sequence of EPO (Nature (1985), Vol. 313,
 CC p. 806). The sequence between nucleotides 63 and 714 has 100% homo-
 CC logy with the published sequence. It encodes the 166 AAs of the
 CC mature EPO protein and 22 AAs of the leader sequence. This clone
 CC and a second, EPO 125, were used to construct a full length clone
 CC which was expressed in rodent epithelial cells.
 See also P81196.
 Sequence 188 AA;
 SQ

Qy	Db	72	kmvfyawk-rmeyqqavavwqqlallseavrlrqgall 108
		66	DFSIGEMKRTQME-ETKAQDILGAVTLLECVMAARGQQL 102
RE	RESULT	6	
ID	P60597		standard; protein; 193 AA.
AC	P60597;		
DT	01-JAN-1980	(first entry)	
DE	Clone Lambda HEPOFL13 encoding human erythropoietin.		
KW	Erythropoietin; lambda HEPOFL13; recombinant plasmid vector; anaemia; ss.		
MM	murine cell culture; 3T3; CHO; Chinese hamster ovary; ss.		
OS	Homo sapiens		

Db	7	lllelelpqlpulgapplicdsrveyleakeaenitgccehcelenitvpd	66
Qy	7	LIVMLILITARRI-LSSPAPACDLRVLKLRHSHLRSLSQCDEVRLPPTPVLPVAV	655
Db	67	kunfyawk-rmeyqqavewqgiallseavrqgall	103
Qy	66	DFSLGEWKTQME-ETKAQDITGAVTLLLEGVMARQQL	102

ID R65499 standard; Protein; 193 AA.
 AC R65499;
 DT 24-JUN-1995 (first entry)
 DE Human prepro-erythropoietin.
 KW Erythropoietin; therapeutic; ss.
 OS Synthetic.

CC A recombinant plasmid vector expressing this clone is expressed in e.
CC erythropoietin is useful
CC g 3T3 or CHO cell cultures. The produced erythropoietin is useful
CC for treatment of anaemia, especially renal anaemia. The cloned gene
CC expresses high levels of the protein and thus provides a means of
CC mass production. See also N60514-21 and P60598-99.
SQ Sequence 193 AA;

PT Erythropoietin analogues – useful for treatment of anaemia and have enhanced erythropoietic effect.
PS Disclosure: Page 38-39; 56pp; English.
CC DNA encoding human prepro-erythropoietin may be located into an expression vector for erythropoietin expression in a CHO cell culture. Site-directed mutagenesis may be used in the construction of EPO analogues with improved activity, which may be used in pharmaceutical compositions for inducing erythropoiesis and treating anaemia.
CC Sequence 193 AA;
50

PD 02-MAY-1991.

PF 09-OCT-1990; US5758.

PR 13-OCT-1989; US-421444.

PA (AMGE-) AMGEN INC.

PI Strickland TW, Byrne TE, Elliott SG;

DR WPI; 91-148745/20.

DR WPI; 91-150265/21.

PT Recombinant erythropoietin iso-forms and purification. - increase haemocrit levels in mammals and contg. specific number of sialic acids

PS Claim 33; Page 45; 60pp; English

The analogue was constructed to add an O-glycosylation site at Thr125 (amino acid 154 in the sequences) and was produced by expression of DNA obtained by site-directed mutagenesis of DNA encoding EPO. The analogue has a higher sialic acid content than human EPO and has increased biological activity.

CC It can be used to treat mammals to cause bone marrow cells to increase prodn. of reticulocytes and red blood

CC thereby increasing haemocrit levels.

CC See also R11859, R11891-93.

SQ Sequence 193 AA;

Query Match 5.7%; Score 141; DB 2; Length 193;

Best Local Similarity 27.6%; Pred. No. 5.15e-02;

Matches 27; Conservative 27; Mismatches 41; Indels 3; Gaps 3;

Db 12 llisllslplglpvlgapprlcsdrvrlleakeenittgcaehcnenitvpdt 71

||: :| | - |::|:|| || ||| :| :: :|:| :| :|

Qy 7 LIVVMILLTARLT-JSSPAPACDLRVLISKLRLDSHVLHSRLSQCPEVHPLPVPVLPVLPAV 65

Db 72 knfyaw-k-rmavqgavewqglalleavrlqgall 108

||: ||::| | :| ::|| |::| |::|

Qy 66 DFSIGEMKIQME-ETKAQDILGAVTLLLEGVMAARGQI 102

RESULT 8

ID P50300 standard; protein; 193 AA.

AC P50300.

DT 01-JAN-1980 (first entry)

DE Human erythropoietin encoded by positive clone (phage lambda-hE1)

DE isolated from human fetal liver gene bank.

DE Erythropoietin; red blood cell; erythrocyte; anaemia; blood;

DE disorder; ss; phage lambda-hE1; gene bank.

OS Homo sapiens.

PN W08507610-A.

PD 20-JUN-1985.

PR 11-DEC-1984; U02021.

PR 13-DEC-1983; US-561024.

PR 21-FEB-1984; US-582185.

PR 28-SEP-1984; US-655841.

PR 30-NOV-1984; US-675298.

PA (KIRI-) KIRIN-AMGEN INC.

DR WPI; 85-159229/26.

DR N-PSDB; N50345.

PT New polypeptide having properties of erythropoietin - is prep'd. by cultivation of transformed eucaryotic or procarcyotic host

PS Disclosure; Page 43; 113pp; English.

CC Human erythropoietin encoded by a sequence encoded by this phage lambda-hE1 is essential for red blood cell formation and is used for the diagnosis and treatment of blood disorders such as anaemia. Large amounts of EPO may be obtained using recombinant DNA techniques in contrast to small amounts obtained from plasma and urine. This sequence is expressed in E. coli. See also N50345-6, N50348-50 and P50298-99, P50301.

SQ Sequence 193 AA;

Query Match 5.7%; Score 141; DB 2; Length 193;

Best Local Similarity 27.6%; Pred. No. 5.15e-02;

Matches 27; Conservative 27; Mismatches 41; Indels 3; Gaps 3;

Db 12 llisllslplglpvlgapprlcsdrvrlleakeenittgcaehcnenitvpdt 71

||: :| | - |::|:|| || ||| :| :: :|:| :| :|

Qy 7 LIVVMILLTARLT-JSSPAPACDLRVLISKLRLDSHVLHSRLSQCPEVHPLPVPVLPVLPAV 65

Db 72 knfyaw-k-rmavqgavewqglalleavrlqgall 108

||: ||::| | :| ::|| |::| |::|

Qy 66 DFSIGEMKIQME-ETKAQDILGAVTLLLEGVMAARGQI 102

RESULT 10

ID R23016 standard; Protein; 330 AA.

AC R23016.

DT	20-OCT-1992	(first entry)
DE	Epo:IL-3 short, recombinant hematopoietic molecule.	
KW	Early MDF; late MDF; haematopoiesis; Epo; IL-3; growth factor.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	Peptide	1..27
FT	/label= sig_peptide	
FT	Protein	28..330
FT	/label= mat_protein	
PN	W09206116-A.	
PD	16-APR-1992.	
PF	26-SEP-1991; U07053.	
PR	28-SEP-1990; US-589958.	
PA	(ORTHO) ORTHO PHARM CORP.	
PI	Rosen JI;	
DR	WPI; 92-150819/18.	
DR	N-PSDB; Q24282.	
PT	Recombinant hematopoietic molecules useful in treating anaemia(s) - comprise IL-3 or GM-CSF, EPO, G-CSF, IL-5 or M-CSF and has early and later myeloid differentiation activity	
PS	Disclosure; Page 44; 82pp; English.	
CC	The amino acid sequence given is an Epo:IL-3 hybrid growth factor derived from a construction formed by ligating the native Epo signal sequence and various synthetic oligonucleotides corresponding to Epo and IL-3 gene sequences. This hybrid growth factor is a haematopoietic molecule which contains at least a portion of an early MDF and at least	
CC	portion of a late MDF covalently linked. This compound can be used to promote hematopoiesis in a patient.	
CC	The bonding of the early and late factors allows a very high conc. of late MDF at the surface of a cell which the early MDF is bound. It also allows the early MDF to act more specifically to stimulate only the desired lineage, thus reducing undesirable effects. These compounds are useful for treating anaemias of various origins e.g. renal failure and AIDS. It is easier to produce and administer one recombinant molecule rather than two separate molecules.	
CC	given in R33065 and contains a flexible linker molecule. This hybrid growth factor is a haematopoietic molecule which contains at least a portion of an early MDF and at least a portion of a late MDF covalently linked. This compound can be used to promote hematopoiesis in a patient.	
CC	The bonding of the early and late factors allows a very high conc. of late MDF at the surface of a cell which the early MDF is bound. It also allows the early MDF to act more specifically to stimulate only the desired lineage, thus reducing undesirable effects. These compounds are useful for treating anaemias of various origins e.g. renal failure and AIDS. It is easier to produce and administer one recombinant molecule rather than two separate molecules.	
SQ	Sequence 330 AA;	
Query Match	5.7%; Score 141; DB 4; Length 330;	
Best Local Similarity	27.6%; Pred. No. 5.15e-02;	
Matches	27; Conservative 27; Mismatches 41; Indels 3; Gaps 3;	
Db	12 llslslslplqlpvlgapprllcslsrlvrlleakeaenittgcaehsclmenitvpdt 71	
Qy	1 llvllmltlarlr-lssppappcldrlvlsklrldshvlhslrsllsqcpevhrlptpvlipav 65	
Db	72 kvnfyawk-r-mevqgqavewqgallseavirgqall 108	
Qy	66 DFSLGENKTMEE-ETRAQDILGAVTILLEGVMARQQL 102	
RESULT	11	
ID	R23079 standard; Protein; 349 AA.	
AC	R23079;	
DT	20-OCT-1992 (first entry)	
DE	Epo:IL-3 Flex, recombinant hematopoietic molecule.	
KW	Early MDF; late MDF; haematopoiesis; Epo; IL-3; linker; growth factor.	
OS	Homo sapiens.	
Key	Location/Qualifiers	
FT	Peptide	1..27
FT	/label= sig_peptide	
FT	Protein	28..349
FT	/label= mat_protein	
PN	W09206116-A.	
RESULT	12	
ID	R06058 standard; protein; 193 AA.	
AC	R06058;	
DT	01-JAN-1980 (first entry)	
DE	Open reading frame coding for the erythropoietin tryptic fragment of lambda REPO1.	
KW	Erythropoietin; lambda REPO1; recombinant plasmid vector; anaemia; mammal cell culture; 3T3; CHO; Chinese hamster ovary; ss. OS Homo sapiens.	
PN	W08603520-A.	
PD	19-JUN-1986	
PF	03-DEC-1985; U02405.	
PR	04-DEC-1984; US-677813.	
PR	03-JAN-1985; US-688622.	
PR	22-JUN-1985; US-693258.	
PA	(GENE-) GENETICS INST INC.	
PA	(FRIV-) FRITSCHIE E.	
PI	Fritsch E, Hewick RM, Jacobs K;	
DR	WPI; 86-169459/26.	
DR	N-PSDB; N60518.	
PT	Prodn. of erythropoietin, useful for treating anaemia	
PT	prodn. of erythropoietin, useful for mass	

REFERENCE JC4125
 #authors Ogami, K.; Shimada, Y.; Sohma, Y.; Akahori, H.; Kato, T.;
 #journal Kawamura, K.; Miyazaki, H.
 Gene (1995) 158:309-310
 #title The sequence of a rat cDNA encoding thrombopoietin.

#accession JC4125
 #status preliminary
 #residues 1-326 #label oca
 #cross-references DDBJ:D32207

SUMMARY #length 326 #molecular-weight 34556 #checksum 730
 Query Match 68.6%; Score 1711; DB 13; Length 326;
 Best Local Similarity 76.0%; Pred. No. 1.06e-142;
 Matches 241; Conservative 43; Mismatches 31; Indels 2; Gaps 2;

Db 1 meltddilvailtaritlspyppacdpdklklrdsylhsrisqqdpnpliy 60
 Qy 1 MELTELLIVVMILLARLITLSSPAPPACDILRVLKLRDLSHLHSRISQDPENHPLPYV 60

Db 61 llpavdfsiegwtktqteqskaqdilgavsllelgymargqlepcscslllgisqvr 120
 Qy 61 LLPAVDFSIEGWTKTQTEQSKAQDILGAVSLLELGYMARGQLEPCSCSLLLGISQVR 120

Db 121 llgalqqlgtqppggttahkdpsafslfllqqlgkqrflvflvegapcvrtlpt 180
 Qy 121 LLLGALQSLGTQPPGQTAAKDLPSAFSLFLLQQLGKQRFLVFLVEGAPCVRTLPT 180

Db 181 avpstsqqlinkfpnrtsglletnfavartagplnlrqfraklqpgqinqtsge 240
 Qy 181 AVPSTSQQLINKFPNRTSGLLETNFAVARTAGPLNLRQFRAKLPGLNQTSRS 239

Db 241 lqiqgqyglngtheppngqhgfaastlqtleaptwvpgatnkgplnlgsgipppia 300
 Qy 240 LQIQGQYGLNGTHEPPNGQHGFAASTLQTLTEAPTWVPGATNKGPLNLGSQPIH 299

Db 301 acg-ytlfppspftptp 316
 Qy 300 PGQYTLFPLPPTP 316

RESULT

5

ENTRY A55530 #type complete
 TITLE megakaryocyte growth and development factor, long form -
 human

ALTERNATE_NAMES MPL ligand, long form
 ORGANISM #formal_name Homo sapiens #common_name man
 DATE 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change
 31-Mar-1995

ACCESSIONS A55530
 REFERENCE Chang, M.; McNinch, J.; Basu, R.; Shutter, J.; Hsu, R.;
 Perkins, C.; Mar, V.; Sugis, S.; Welcher, A.; Li, L.; Lu, H.; Bartley, T.; Hunt, P.; Martin, F.; Samal, B.; Bogenberger, J. J. Biol. Chem. (1995) 270:511-514
 #journal Cloning and characterization of the human megakaryocyte
 #title growth and development factor (MGDF) gene.
 #accession A55530

#status Preliminary; not compared with conceptual translation
 #molecule_type DNA
 #residues 1-286 #label CHA
 #cross-references GB:U17071

#map_position 3426.3
 #keywords alternative splicing; cytokine
 #length 286 #molecular-weight 31544 #checksum 6126
 SUMMARY

Query Match 45.8%; Score 1143; DB 10; Length 286;
 Best Local Similarity 94.2%; Pred. No. 1.05e-142;
 Matches 163; Conservative 2; Mismatches 6; Indels 2; Gaps 2;

Db 1 meltddilvailtaritlspyppacdpdklklrdsylhsrisqqdpnpliy 60
 Qy 1 MELTELLIVVMILLARLITLSSPAPPACDILRVLKLRDLSHLHSRISQDPENHPLPYV 60

Db 61 llpavdfsiegwtktqteqskaqdilgavsllelgymargqlepcscslllgisqvr 120
 Qy 61 LLPAVDFSIEGWTKTQTEQSKAQDILGAVSLLELGYMARGQLEPCSCSLLLGISQVR 120

Db 121 llgalqqlgtqppggttahkdpsafslfllqqlgkqrflvflvegapcvrtlpt 171
 Qy 121 LLLGALQSLGTQPPGQTAAKDLPSAFSLFLLQQLGKQRFLVFLVEGAPCVRTLPT 171

Db 181 avpstsqqlinkfpnrtsglletnfavartagplnlrqfraklqpgqinqtsge 240
 Qy 181 AVPSTSQQLINKFPNRTSGLLETNFAVARTAGPLNLRQFRAKLPGLNQTSRS 239

Db 241 lqiqgqyglngtheppngqhgfaastlqtleaptwvpgatnkgplnlgsgipppia 300
 Qy 240 LQIQGQYGLNGTHEPPNGQHGFAASTLQTLTEAPTWVPGATNKGPLNLGSQPIH 299

Db 301 acg-ytlfppspftptp 316
 Qy 300 PGQYTLFPLPPTP 316

RESULT

6

ENTRY A24902 #type complete
 TITLE erythropoietin precursor - mouse
 ORGANISM #formal_name Mus musculus #common_name house mouse

ACCESSIONS A24902
 #authors Shoemaker, C.B.; Mitnick, L.D.
 #journal Mol. Cell. Biol. (1986) 6:849-858
 #title Murine erythropoietin gene: cloning, expression, and human
 #cross-references MIM:87039105
 #accession A24902

#molecule_type DNA
 #residues 1-192 #label SHO
 #note the authors translated the codon TAA for residue 12 as
 Phe, TTA for residue 43 as Phe and ATC for residue 145
 as Ile

GENETICS

#introns 5/1; 52/3; 81/3; 141/3
 #classification #superfamily erythropoietin
 #keywords erythropoiesis; glycoprotein; hormone

SUMMARY #length 192 #molecular-weight 21339 #checksum 6155

Query Match 6.2%; Score 155; DB 5; Length 192;
 Best Local Similarity 26.8%; Pred. No. 3.6e-05;
 Matches 34; Conservative 35; Mismatches 54; Indels 4; Gaps 4;

Db 10 llilslillplglpvcaprlcdsrrlyleakeaenvtgcaeqrlsentrivad 69
 Qy 6 LLLVLLMLLARLT-LS-SPAPCQLRVLKLRDLSHLHSRISQDPENHPLPYV 64

Db 70 tknfyawk-rmeyeqaqiawqglslsealqagallanssppatqlqhdkaisq 128
 Qy 65 VDPSLDEMKTQE-ETKAQDILGAVTLLLEGVMARGQLEPCSCSLLLGISQVR-L 122

Db 129 rsltsll 135
 Qy 123 GAQSLL 129

GENETICS
 #gene MCDF

ENTRY	S28148	TYPE	#type complete
		ORGANISM	erythropoietin - rat
		NAME	#formal_name Rattus norvegicus #common_name Norway rat
		DATE	22-Nov-1993 #sequence_revision 22-Nov-1993 #text_change
ACCESSIONS	S28148		
REFERENCE		authors	Nagao, M.; Suga, H.; Okano, M.; Masuda, S.; Narita, H.; Ikuwa, K.; Sasaki, R.
		journal	Biochim. Biophys. Acta (1992) 1171:99-102
		title	Nucleotide sequence of rat erythropoietin.
accession	S28148	status	#status preliminary
		residues	#length 192 #label NAC
SUMMARY			
		Query Match	6.2%; Score 154; DB 13; Length 192;
		Best Local Similarity	25.8%; Pred. No. 4.65e-05;
		Matches	34; Conservative 35; Mismatches 58; Indels 5; Gaps 5;
Db	10	lillslplgplgvicaprldcdrvryleakeaenvtmgaeprisnitvpd	69
Qy	6	ll	64
Db	70	tknfyawkkmkkveeqavewqqlsllseailqagqlqanssppesqlqhdkaig	129
Qy	65	vdpslgkwtkomeetkraqdilgavtlllegwmaarg-qlcpt-clslsqlgsgqr-l	121
Db	130	stslslrlvlgq	141
Qy	122	-lgaloqslgtq	132
RESULT	8		
ENTRY		TYPE	#type complete
TITLE		NAME	erythropoietin precursor - human
ORGANISM		FORMAL_NAME	Homo sapiens #common_name man
DATE		27-Nov-1985 #sequence_revision 27-Nov-1985 #text_change	22-Apr-1995
ACCESSIONS	A01855; A24744; A25384; A22210		
REFERENCE		authors	Jacobs, K.; Shoemaker, C.; Rudersdorf, R.; Neill, S.D.; Kaufman, R.J.; Mufson, A.; Seehra, J.; Jones, S.S.; Hewick, R.; Fritsch, E.F.; Kawakita, M.; Shimizu, T.; Miyake, T.
		journal	Nature (1985) 313:806-810
		title	Isolation and characterization of genomic and cDNA clones of human erythropoietin.
#cross-references	W01D:85137809		
accession	A01855		
		type	#molecule_type mRNA; DNA
		residues	1-193 #label JAC
		cross-references	GB:X02157; GB:X02158
REFERENCE	A24744		
		authors	Lin, F.K.; Sugge, S.; Lin, C.H.; Browne, J.K.; Shallowitz, R.; Egrie, J.C.; Chen, K.K.; Fox, G.M.; Martin, F.; Stabinsky, Z.; Badawi, S.M.; Iai, P.H.; Goldwasser, E.
		journal	Proc. Natl. Acad. Sci. U.S.A. (1985) 82:7580-7584
		title	Cloning and expression of the human erythropoietin gene.
#cross-references	W01D:85067948		
accession	A24744		
		type	#molecule_type DNA
		residues	1-193 #label LIN
		cross-references	GB:MI1319
REFERENCE	A23384		
RESULT	9		
ENTRY		TYPE	#type complete
TITLE		NAME	annexin XI - rabbit
ALTERNATE_NAMES		FORMAL_NAME	calcyclin-associated annexin protein CAP-50
ORGANISM		COMMON_NAME	domestic rabbit
DATE		20-Nov-1993 #sequence_revision 30-Sep-1993 #text_change	30-Feb-1995
ACCESSIONS	JH0694; PH0050; A38250; PS0263		
REFERENCE		authors	Komatsu, H.; Mizutani, A.; Muramatsu, M.; Yokota, T.; Arai, K.; Hidaka, H.


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# residues 1-350 #label RAZ
#cross-references EMBL:64173
KEYWORDS glycoprotein; hydroxyproline
#length 350 #molecular-weight 36721 #checksum 6552
#SUMMARY

Query Match 4.9%; Score 121; DB 9; Length 350;
Best Local Similarity 40.7%; Pred. No. 1.35e-01;
Matches 24; Conservative 4; Mismatches 29; Indels 2; Gaps 2;
Db 82 pyptpsiptppt-ytpptptp-pkptppytppapphkptptpkptppytppk 138
Qy 290 RPPSPSPTRHPTGQTYLPLPPLPTPVQQLPLPPLPDSAPTPTPSP 348

RESULT 15
ENTRY #type complete
TITLE annexin XI - human
ORGANISM #common name man
DATE 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change
25-Aug-1995

ACCESSIONS A53152
REFERENCE A53152
Authors Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; van
Venrooij, W.J.
Journal J. Biol. Chem. (1994) 269:4240-4246
Title The 56K autoantigen is identical to human annexin XI.
Accession A53152
#status preliminary
#molecule_type mRNA
#residues 1-505 #label MTS

CLASSIFICATION #superfamily annexin repeat homology
#cross-references GB:119605
#molecule_type mRNA

FEATURE 203-214
358-370
SUMMARY #domain annexin repeat homology #label AX1\
#domain annexin repeat homology #label AX3
#length 505 #molecular-weight 54389 #checksum 1160

Query Match 4.9%; Score 121; DB 10; Length 505;
Best Local Similarity 24.8%; Pred. No. 1.35e-01;
Matches 25; Conservative 29; Mismatches 41; Indels 6; Gaps 6;
Db 38 qldnvatyagqfnodysgmaamnsgtfgaa-mpnlypapdag-yppppppgfgqps 95
Qy 239 SLDQPGYLNRI-HELLNGTRGLFPGRSRRTLGAPDIISSGTSQGSLPQLQPGIS-PSP 296

Db 96 aequppppqmp-ppq-qnppasppspppppgavvppqmp 134
Qy 297 THPPGQTYLPLPPLPTPVPVQQLPLPPLPDSAPTPTPSP 337

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[1] SEQUENCE FROM N.A.
 RP SEQUENCE FROM N.A.
 RP 87039105
 RA SHOEMAKER C.B., MITSOCK L.D.,
 RL MOL. CELL. BIOL. 6:899-958 (1986).
 RL (2)
 RN SEQUENCE FROM N.A.
 RM 87039104
 RA MCDONALD J.D., LIN F.-K., GOLDMASSER E.,
 RL MOL. CELL. BIOL. 6:842-948 (1986).
 CC -!- FUNCTION: ERYTHROPOETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
 CC REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A
 CC PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.
 CC -!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
 CC AND BY LIVER OF FETAL OR NEONATAL MAMMALS.
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 DR EMBL; M14982; EMBR.
 DR EMBL; M12930; MMERPA.
 DR PIR; A24901; A24901.
 DR PIR; A24902; A24902.
 DR PROSITE; PS00817; EPO.
 KW ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 22
 CC BY SIMILARITY.
 FT CHAIN 23 188
 CC ERYTHROPOETIN.
 FT DISULFID 29 183
 CC BY SIMILARITY.
 FT DISULFID 51 55
 CC BY SIMILARITY.
 FT CARBOHYD 46 46
 CC POTENTIAL.
 FT CARBOHYD 60 60
 CC POTENTIAL.
 FT CARBOHYD 105 105
 CC POTENTIAL.
 SQ SEQUENCE 188 AA; 20608 MW; 175419 CN;
 DR EMBL; M13027; FCERHYRO.
 DR PROSITE; PS00817; EPO.
 KW ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 22
 CC BY SIMILARITY.
 FT CHAIN 23 188
 CC ERYTHROPOETIN.
 FT DISULFID 29 183
 CC BY SIMILARITY.
 FT DISULFID 51 55
 CC BY SIMILARITY.
 FT CARBOHYD 46 46
 CC POTENTIAL.
 FT CARBOHYD 60 60
 CC POTENTIAL.
 DR EMBL; M13027; FCERHYRO.
 DR PROSITE; PS00817; EPO.
 KW ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 22
 CC BY SIMILARITY.
 FT CHAIN 23 188
 CC ERYTHROPOETIN.
 FT DISULFID 29 183
 CC BY SIMILARITY.
 FT DISULFID 51 55
 CC BY SIMILARITY.
 FT CARBOHYD 46 46
 CC POTENTIAL.
 FT CARBOHYD 60 60
 CC POTENTIAL.
 DR EMBL; M13027; FCERHYRO.
 DR PROSITE; PS00817; EPO.
 KW ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 22
 CC BY SIMILARITY.
 DR EMBL; M13027; FCERHYRO.
 DR PROSITE; PS00817; EPO.
 KW ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.
 FT NON TER 1 1
 FT SIGNAL <1 22
 CC BY SIMILARITY.

Query Match 6.2%; Score 155; DB 3; Length 175;
 Best Local Similarity 25.2%; Pred. No. 3.5e-07;
 Matches 32; Conservative 39; Mismatches 52; Indels 4; Gaps 4;
 Sq 175 AA; 191.93 MW; 155009 CN;

Db 6 lllllllllplglpvlgapprlicsdrvleyleareaaenvtngcaggcaffenitvpd 65
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 6 lllllllllplglpvlgapprlicsdrvleyleareaaenvtngcaggcaffenitvpd 64
 |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 66 tkvnfytwk-rndvqgalerwqglallseailrqgallanasqspsetpqhdkvssl 124
 ::|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Qy 65 VDFSLGEMKTOME-ETKAQDILGAVTILLEGMAARGOLGPTCLLSLIGQSVRVL-L 122
 DE 125 raltsll 131
 Qy 123 GALQSL 129

RESULT 6

ID	EPO RAT	STANDARD;	PRT;	192 AA.
AC	P29576			
DT	01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	ERYTHROPOETIN PRECURSOR.			
GN	EPO.			
OS	RATTUS NORVEGICUS (BAT).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
RN	1] EUKARYOTA; ROTENTA.			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=WISTAR; TISSUE=KIDNEY;			
RM	93042015			
RA	NAGAO M., SUGA H., MASUDA S., NARITA H., IKURA K., SASAKI R.; RYUJI RYUJI BIOCIM. BIOPHYS. ACTA 1171:99-102(1992).			
CC	CC -!- FUNCTION: ERYTHROPOETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.			
CC	-!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS AND BY LIVER OF FETAL OR NEONATAL MAMMALS.			
CC	-!- SUBCELLULAR LOCATION: SECRETED.			
DR	EMBL; D10763; RNPO.			
DR	PIR; S28148; S28148.			
DR	PROSITE; PS00817; EPO.			
KW	ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.			
FT	SIGNAL 1 26 BY SIMILARITY.			
FT	CHAIN 27 192 BY ERYTHROPOETIN.			
FT	DISULFID 33 187 BY SIMILARITY.			
FT	CARBOHYD 50 50 BY SIMILARITY.			
FT	CARBOHYD 64 64 BY SIMILARITY.			
FT	CARBOHYD 109 109 BY SIMILARITY.			
SQ	SEQUENCE 192 AA; 21286 MW; 179242 CN;			

Query Match 6.2%; Score 154; DB 3; Length 192;
 Best Local Similarity 25.8%; Pred. No. 4.8e-07;

RESULT 7

ID	EPO HUMAN	STANDARD;	PRT;	193 AA.
AC	P01588			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DE	ERYTHROPOETIN PRECURSOR.			
GN	EPO.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	1] SEQUENCE FROM N.A.			
RP	SEQUENCE FROM N.A.			
RA	JACOBS K., SHOEMAKER C., RUDERSDORF R., NEILL S.D., KAUFMAN R.J., RA MUFSON A., SEEHER J., JONES S.S., HEMICK R., FRITSCH E.F., RA KAWAKITA M., SHIMIZU T., MIYAKE T.; RAL NATURE 313:806-810(1985).			
RN	2] SEQUENCE FROM N.A.			
RA	LIN F.-K., SUGGS S., LIN C.-H., BROWNE J.K., SMALLING R., EGRIE J.C., CHEN K.K., FOX G.M., MARTIN F., STABINSKY Z., BADRANI S.M., LAI P.-H., RA GOLDWASSER E.; RAL PROC. NATL. ACAD. SCI. U.S.A. 82:7580-7584(1985).			
RN	3] SEQUENCE OF 28-193, AND DISULFIDE BONDS.			
RC	TISSUE=IRINE;			
RM	86140080			
RA	LAI P.H., EVERETT R., WANG F.F., ARAKAWA T., GOLDWASSER E.; RA GOTO M.; RAL. CHEM. 26:1316-1321(1986).			
RN	4] PRELIMINARY SEQUENCE OF 28-57.			
RP	PRELIMINARY SEQUENCE OF 28-57.			
RM	84135751			
RA	YANAGAWA S., HIRADE K., OHNOMA H., SASAKI R., CHIBA H., UEDA M., RA KOBAYA A.; RAL. J. BIOL. CHEM. 263:3657-3663(1988).			
RL	J. BIOL. CHEM. 259:2707-2710(1984).			
RN	5] STRUCTURE OF CARBOHYDRATES.			
RM	88155657			
RA	TAKEUCHI M., TAKASAKI S., MIYAZAKI H., KATO T., HOSHI S., KOCHIBE N., RA KOBAYA A.; RAL. J. BIOL. CHEM. 263:3657-3663(1988).			
RN	6] STRUCTURE OF CARBOHYDRATES.			
RM	89118279			
RA	SASAKI H., OCHI N., DELI A., FUKUDA M.; RAL. BIOCHEMISTRY 27:8618-8626(1988).			
RN	7]			

Query Match		5.6%	Score 139;	DB 1;	Length 503;
Best Local Similarity		25.7%	Pred. No. 4	88-05;	
Matches		26	Conservative	0	Mismatches 41; Indels 4; Gaps 4;
RESULT	9				
ID	EPO SHEEP	STANDARD;	PRT;	194 AA.	
AC	P33759;				
DT	01-FEB-1994 (REL. 28, CREATED)				
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)				
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)				
DE	ERYTHROPOIETIN PRECURSOR.				
GN	EPO.				
OS	OVIS ARIES (SHEEP).				
OC	EKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;				
OC	EUTHERRIA; ARTIODACTYLA.				
[1]					
RN	SEQUENCE FROM N.A.				
RC	TISSUE=KIDNEY;				
RM	93351736				
RA	FO P., EVANS B., JIM G.B., MORITZ K., WINTOUR M.E.;				
RL	MOL. CELL. ENDOCRINOL. 93:107-116 (1993).				
CC	-!- FUNCTION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE REGULATION OF ERYTHROCYTE DIFFERENTIATION AND THE MAINTENANCE OF A PHYSIOLOGICAL LEVEL OF CIRCULATING ERYTHROCYTE MASS.				
CC	-!- TISSUE SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS AND BY LIVER OF FETAL OR NEONATAL MAMMALS.				
CC	-!- SUBCELLULAR LOCATION: SECRETED.				
DR	EMBL; 224681; OXENPOIA.				
DR	PROSITE; PS00817; EPO.				
KW	ERYTHROCYTE MATURATION; GLYCOPROTEIN; HORMONE; SIGNAL.				
FT	SIGNAL 1 27 BY SIMILARITY.				
FT	CHAIN 28 194 ERYTHROPOIETIN.				
FT	DISULFID 34 189 BY SIMILARITY.				
FT	DISULFID 56 60 BY SIMILARITY.				
FT	CARBONYD 51 51 POTENTIAL.				
FT	CARBONYD 65 65 POTENTIAL.				
FT	CARBONYD 110 110 POTENTIAL.				
SQ	SEQUENCE 194 AA; 21335 MM; 175348 CN;				

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best local Similarity 25.0%;
 Pred. No. 6.39e-05;
 Matches 25; Conservative
 32; Mismatches 40; Indels 3; Gaps 3;

SCIMIDAE; METACELARIS (CRAB EATING MACAQUE); METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA; PRIMATES

6 LLLVVMLLRLT-LSSAPPACDYLRSKLRLDSHLVLSRLSCLSCPEVHPLPTVLLPA 64
71 tkvnfyawk-rmeyqqgalewqgjaliseairfgqalla 109
:: || :| :| ::|| |::| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
65 VDSELGERKTMQE-ETKQDPLGAVTLLEGWMARQGLG 103

FROM N.A.
, LIN C.-H., LAI P.-H., BROWNE J.K., EGRIE J.C., SMALLING R.,
CHEN K.K., CASTRO M., SUGGS S.;
01-2094(1986).
TION: ERYTHROPOIETIN IS THE PRINCIPAL HORMONE INVOLVED IN THE
ON AN ERYTHROPOEtic HEMOGLOBIN. ANNUAL MEETING OF THE AMERICAN
1986.

RESULT 10
ID SSGP VOLCA STANDARD; PRT; 485 AA.

SPECIFICITY: PRODUCED BY KIDNEY OR LIVER OF ADULT MAMMALS
BY LIVER OF FETAL OR NEONATAL MAMMALS.

OC OC
 EUKARYOTA; PLANTAE; PHYLLOPHYTA; CHLOROPHYTA (GREEN ALGAE);
 CHLOROPHYCEAE; VOLVOCALES; VOLVOACEAE.
 [1]
 RN RN
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC RC
 STRAIN=F. NAGARTENSIS / HK 10;
 RM 90094551
 RA ERTL H., MENGELE R., WENZEL S., ENGEL J., SUMPER M.;
 RL J. CELL BIOL. 109:3493-3501 (1989).
 CC CC
 -!- FUNCTION: THE EXTRACELLULAR MATRIX (ECM) OF VOLVOX CONTAINS
 INSOLUBLE FIBROUS LAYERS THAT SURROUND INDIVIDUAL CELLS AT A
 DISTANCE TO FORM CONTIGUOUS CELLULAR COMPARTMENTS. SSG 185 IS THE
 MONOMERIC PRECURSOR OF THIS SUBSTRUCTURE (C32 STRUCTURE). THE
 COVALENT CROSS-LINKS ARE FORMED BETWEEN THE SACCHARIDE CHAINS
 RATHER THAN BETWEEN THE POLYPEPTIDE CHAINS.
 CC CC
 -!- PTM: A CENTRAL DOMAIN OF 77 AA CONSISTS ALMOST EXCLUSIVELY OF
 HYDROXYPROLINE RESIDUES.
 CC CC
 PIR; A33647; A33647.
 DR DR
 HSSP; P19991; ICLG.
 KW KW
 GLYCOPROTEIN; SULFATION; HYDROXYLATION.
 FT FT
 DOMAIN 228 340 PRO-RICH.
 FT DOMAIN 260 295 POLY-PRO.
 SQ SEQUENCE 485 AA; 50436 MW; 1322558 CN;
 SEQUENCE 485 AA; 50436 MW; 1322558 CN;
 Query Match 5.3%; Score 132; DB 7; Length 485;
 Best Local Similarity 33.8%; Pred. No. 3.90e-04;
 Matches 24; Conservative 20; Mismatches 24; Index 3; Caps 3;
 DOMAIN 260 295 POLY-PRO.
 SEQUENCE 485 AA; 50436 MW; 1322558 CN;
 SEQUENCE 485 AA; 50436 MW; 1322558 CN;
 Db 212 Iaqgnvnpiqapapinsplpsppqtaasrpssppsprrpsppppps-pspppppppppp
 ||:||||: ||:: :||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
 Qy 269 IAGADDSS-G-TSDTGSLLPNLQPGYSPSPTHPPTGQYTLRPLPPTLPVQLHPLPD 326
 Db 271 PPPPPPPPPP 281
 |:||:||:||:
 Qy 327 PSADPTPTPPTSP 337

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CC - TISSUE SPECIFICITY: EXPRESSED IN A WIDE VARIETY OF TISSUES.
CC - DOMAIN: CONTAINS FOUR HOMOLOGOUS REPEATS WITH A CONSENSUS
CC SEQUENCE COMMON TO ALL ANNEXIN PROTEINS. A PAIR OF THESE REPEATS
CC MAY FORM ONE BINDING SITE FOR CALCIUM AND PHOSPHOLIPID.
CC - SIMILARITY: TO OTHER PROTEINS OF THE ANNEXIN FAMILY.
CC - ALTERNATIVE PRODUCTS: TWO FORMS OF ANNEXIN XI ARE PRODUCED BY
CC ALTERNATIVE SPLICING OF THE SAME GENE.
EMBL: M82807; BLANXIS.
DR PIR: A42113; IUBOI1.
DR PIR: A42113; IUBOI1.

Db	374	pptlapplpattpppn-kassumpapppppppgffstssalsasasiplapl--pppppp	431
Qy	271	ADPISSTSBTGSLPENLQPGYSPSPRHPTGOTYLFPLPPTPTVYQVQLHPLPSP	330
Db	432	svatvpp	438
Qy	331	TPPTSP	337

DE 90-100-1394 (REL. 30, LASI ANNOUNCEMENT UPDATE)
 DE HYPOTHETICAL 49.6 KD PROTEIN IN FBAL-T0A.2 INTERGENIC REGION.
 GN YKL05C OR YKL136.
 OS SACCHAROMYCES CERESIAE (BAKER'S YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOMYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RM 94378723
 RA RASMUSSEN S. W.;
 RL YEAST 10:S62-S68 (1994).

RESULT 13
 ID VRP1 YEAST
 AC P37370;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 01-OCT-1994 (REL. 30, LAST ANNOTATION UPDATE)
 DE VERPOLIN.
 GN VRP1.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Query	Match	4.6%; Score 115; DB Pred. No. 4.762
Best Local	Similarity	27.2%; Pred. No. 4.762
Matches	25; Conservative	25; Mismatcheeve

RN
[1]
SEQUENCE FROM N.A.
RC
STRAIN=3364;
RM
95058201
RA
DONNELL S.F.H., POCKLINGTON M.J., PALLOTA D., ORR E.;
RL
MOL. MICROBIOL. 10: 585-596 (1993).
CC
-!- FUNCTION: INVOLVED IN CYTOSKELETAL ORGANISATION AND CELLULAR
GROWTH, MITOSIS, CYTOKINESIS, AND PROLIFERATION.
CC

Db	349 evetflkkqgelelgsskdqnpettkmklnpdgtgaglnntslostsuvngqtpyppyl 408
Qy	242 QICQYNRHIELANGR-GIEGSPSRTGAGDIDSGTSGLSPNQPGCVSPSPTHP- 299
Db	409 pfgippfpmfpmpatit-nphqadasp 439
Qy	300 PTG--QVTLFPLPPTLPFWQHPLRPPSA 329

CC INDIRECTLY VIA PROLINE-BINDING PROTEINS (E.G. PROFILIN) OR
 PROTEINS POSSESSING SH3 DOMAINS.
 EMBL; 226605; SCVRPRL.
 PIR; S33626; S339626.
 DR REPEAT.
 FT DOMAIN 5 14 POLY-PRO.
 FT DOMAIN 239 245 POLY-PRO.
 FT DOMAIN 349 357 POLY-PRO.
 FT DOMAIN 396 406 POLY-PRO.
 FT DOMAIN 424 431 POLY-PRO.
 FT DOMAIN 462 468 POLY-SER.
 FT DOMAIN 704 708 POLY-PRO.
 SQ SEQUENCE 751 AA; 75953 MW; 3267787 CN;

RESULT	15	1874 AA
AC	POLR KYMWJ	STANDARD:
P36304;		
DT	01-JUN-1994 (REL. 29, CREATED)	
DT	01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)	
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)	
DT	RNA. REPICLATE POLYPROTEIN (EC 2.7.7.48).	
OS	KENNEDY YELLOW MOSAIC VIRUS (STRAIN JERVIS	
OC	VIRIDE; SS-RNA NONENVELOPED VIRUSES; TMVOTV	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RM	9021040	
RA	DING S., KESE P., GIBBS A.;	

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Query	Match	Score	DB	Length
Qy	599 alapsplp-yanaplplpypnspfppppplpsqspqspatapaq-ptpgepl	4.6%; 115;	DB 6;	Length 1874;
Db	283 SLPPN-LQPGYSSPRTIP-PTGQTYLIEPLPPTIPPTPVQL-H-PLLEDSAPRTITSLI	40.9%; 8;	Fred. No. 4.76e-02;	
Matches	27; Conservative	8; Mismatches	25; Indels	6; gaps 6;

Qy 339 LNTSYT 344

Search completed: Mon Apr 1 11:00:49 1996
Job time : 25 secs.

JULY 27, 1900